# Neil Q Mcdonald

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7648328/publications.pdf

Version: 2024-02-01

| | | | |
|---|---|---|---|
| 83 papers | 13,615 citations | 53794 45 h-index | 58581 82 g-index |
| 90 all docs | 90 docs citations | 90 times ranked | 22587 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Intratumor Heterogeneity and Branched Evolution Revealed by Multiregion Sequencing. New England Journal of Medicine, 2012, 366, 883-892. | 27.0 | 6,769 |
| 2 | A structural superfamily of growth factors containing a cystine knot motif. Cell, 1993, 73, 421-424. | 28.9 | 525 |
| 3 | New protein fold revealed by a 2.3-Ã... resolution crystal structure of nerve growth factor. Nature, 1991, 354, 411-414. | 27.8 | 500 |
| 4 | The mitochondrial protease HtrA2 is regulated by Parkinson's disease-associated kinase PINK1. Nature Cell Biology, 2007, 9, 1243-1252. | 10.3 | 441 |
| 5 | Disruption of methylarginine metabolism impairs vascular homeostasis. Nature Medicine, 2007, 13, 198-203. | 30.7 | 370 |
| 6 | S -nitrosylation of dimethylarginine dimethylaminohydrolase regulates enzyme activity: Further interactions between nitric oxide synthase and dimethylarginine dimethylaminohydrolase. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 13527-13532. | 7.1 | 278 |
| 7 | Identification of FAAP24, a Fanconi Anemia Core Complex Protein that Interacts with FANCM. Molecular Cell, 2007, 25, 331-343. | 9.7 | 264 |
| 8 | Structural and Functional Relationships of the XPF/MUS81 Family of Proteins. Annual Review of Biochemistry, 2008, 77, 259-287. | 11.1 | 244 |
| 9 | Structure and Chemical Inhibition of the RET Tyrosine Kinase Domain. Journal of Biological Chemistry, 2006, 281, 33577-33587. | 3.4 | 237 |
| 10 | Structural insights into the hydrolysis of cellular nitric oxide synthase inhibitors by dimethylarginine dimethylaminohydrolase. Nature Structural Biology, 2001, 8, 679-683. | 9.7 | 200 |
| 11 | The solution structure of the Josephin domain of ataxin-3: Structural determinants for molecular recognition. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 10493-10498. | 7.1 | 176 |
| 12 | Topological similarities in TGF-Î²2, PDGF-BB and NGF define a superfamily of polypeptide growth factors. Structure, 1993, 1, 153-159. | 3.3 | 152 |
| 13 | A heterozygous effect for PINK1 mutations in Parkinson's disease?. Annals of Neurology, 2006, 60, 414-419. | 5.3 | 149 |
| 14 | Crystal structure of the MAPK phosphatase Pyst1 catalytic domain and implications for regulated activation. Nature Structural Biology, 1999, 6, 174-181. | 9.7 | 141 |
| 15 | The Dual Mechanism of Separase Regulation by Securin. Current Biology, 2002, 12, 973-982. | 3.9 | 131 |
| 16 | A Small-Molecule Inhibitor for Phosphatase and Tensin Homologue Deleted on Chromosome 10 (PTEN). ACS Chemical Biology, 2006, 1, 780-790. | 3.4 | 131 |
| 17 | SAC1 Encodes a Regulated Lipid Phosphoinositide Phosphatase, Defects in Which Can Be Suppressed by the Homologous Inp52p and Inp53p Phosphatases. Journal of Biological Chemistry, 2000, 275, 801-808. | 3.4 | 108 |
| 18 | Structure of Î²2-bungarotoxin: potassium channel binding by Kunitz modules and targeted phospholipase action. Structure, 1995, 3, 1109-1119. | 3.3 | 107 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Structure of an XPF endonuclease with and without DNA suggests a model for substrate recognition. EMBO Journal, 2005, 24, 895-905. | 7.8 | 105 |
| 20 | Nerve growth factor revisited. Trends in Biochemical Sciences, 1993, 18, 48-52. | 7.5 | 94 |
| 21 | 14-3-3 Proteins Interact with a Hybrid Prenyl-Phosphorylation Motif to Inhibit G Proteins. Cell, 2013, 153, 640-653. | 28.9 | 93 |
| 22 | Molecular basis for G-actin binding to RPEL motifs from the serum response factor coactivator MAL. EMBO Journal, 2008, 27, 3198-3208. | 7.8 | 92 |
| 23 | Structure-Function Analysis of Phosphatidylinositol Transfer Protein Alpha Bound to Human Phosphatidylinositol. Structure, 2004, 12, 317-326. | 3.3 | 90 |
| 24 | Structure of a Pentavalent G-Actinâ€¢MRTF-A Complex Reveals How G-Actin Controls Nucleocytoplasmic Shuttling of a Transcriptional Coactivator. Science Signaling, 2011, 4, ra40. | 3.6 | 90 |
| 25 | The three-dimensional solution structure and dynamic properties of the human FADD death domain 1 1Edited by A. Fersht. Journal of Molecular Biology, 2000, 302, 171-188. | 4.2 | 89 |
| 26 | Protein kinase C interventionâ€"the state of play. Current Opinion in Cell Biology, 2009, 21, 268-279. | 5.4 | 88 |
| 27 | Recognition of an intraâ€chain tandem 14â€3â€3 binding site within PKCÎµ. EMBO Reports, 2009, 10, 983-989. | 4.5 | 86 |
| 28 | The Mycobacterium tuberculosis ino1 gene is essential for growth and virulence. Molecular Microbiology, 2004, 51, 1003-1014. | 2.5 | 85 |
| 29 | Structure of a Conserved Dimerization Domain within the F-box Protein Fbxo7 and the PI31 Proteasome Inhibitor. Journal of Biological Chemistry, 2008, 283, 22325-22335. | 3.4 | 83 |
| 30 | Transforming activity of Fbxo7 is mediated specifically through regulation of cyclin D/cdk6. EMBO Journal, 2005, 24, 3104-3116. | 7.8 | 80 |
| 31 | A secondary RET mutation in the activation loop conferring resistance to vandetanib. Nature Communications, 2018, 9, 625. | 12.8 | 75 |
| 32 | Nerve growth factor: Structure/function relationships. Protein Science, 1994, 3, 1901-1913. | 7.6 | 69 |
| 33 | Functional evaluation of tumour-specific variants of p16INK4a/CDKN2A: correlation with protein structure information. Oncogene, 1999, 18, 5423-5434. | 5.9 | 69 |
| 34 | Structure of mouse 7S NGF: a complex of nerve growth factor with four binding proteins. Structure, 1997, 5, 1275-1285. | 3.3 | 68 |
| 35 | Tes, a Specific Mena Interacting Partner, Breaks the Rules for EVH1 Binding. Molecular Cell, 2007, 28, 1071-1082. | 9.7 | 66 |
| 36 | Structural Determinants of Neurotrophin Action. Journal of Biological Chemistry, 1995, 270, 19669-19672. | 3.4 | 65 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | Synthesis, structureâ€“activity relationship and crystallographic studies of 3-substituted indolin-2-one RET inhibitors. Bioorganic and Medicinal Chemistry, 2010, 18, 1482-1496. | 3.0 | 64 |
| 38 | Crystal Structure of Inositol 1-Phosphate Synthase from Mycobacterium tuberculosis, a Key Enzyme in Phosphatidylinositol Synthesis. Structure, 2002, 10, 393-402. | 3.3 | 62 |
| 39 | Localization of Functional Receptor Epitopes on the Structure of Ciliary Neurotrophic Factor Indicates a Conserved, Function-related Epitope Topography among Helical Cytokines. Journal of Biological Chemistry, 1995, 270, 14007-14014. | 3.4 | 58 |
| 40 | aPKC Inhibition by Par3 CR3 Flanking Regions Controls Substrate Access and Underpins Apical-Junctional Polarization. Developmental Cell, 2016, 38, 384-398. | 7.0 | 56 |
| 41 | Oncogenic RET Kinase Domain Mutations Perturb the Autophosphorylation Trajectory by Enhancing Substrate Presentation In trans. Molecular Cell, 2014, 53, 738-751. | 9.7 | 55 |
| 42 | Drugging the catalytically inactive state of RET kinase in RET-rearranged tumors. Science Translational Medicine, 2017, 9, . | 12.4 | 55 |
| 43 | G-actin regulates the shuttling and PP1 binding of the RPEL protein Phactr1 to control actomyosin assembly. Journal of Cell Science, 2012, 125, 5860-5872. | 2.0 | 54 |
| 44 | Adenosine-binding motif mimicry and cellular effects of a thieno[2,3-d]pyrimidine-based chemical inhibitor of atypical protein kinase C isoenzymes. Biochemical Journal, 2013, 451, 329-342. | 3.7 | 51 |
| 45 | RET Recognition of GDNF-GFRÎ±1 Ligand by a Composite Binding Site Promotes Membrane-Proximal Self-Association. Cell Reports, 2014, 8, 1894-1904. | 6.4 | 51 |
| 46 | Focal Adhesion Kinase (FAK) Binds RET Kinase via Its FERM Domain, Priming a Direct and Reciprocal RET-FAK Transactivation Mechanism. Journal of Biological Chemistry, 2011, 286, 17292-17302. | 3.4 | 50 |
| 47 | Mammal-restricted elements predispose human RET to folding impairment by HSCR mutations. Nature Structural and Molecular Biology, 2010, 17, 726-731. | 8.2 | 47 |
| 48 | Identification of tyrosine 806 as a molecular determinant of RET kinase sensitivity to ZD6474. Endocrine-Related Cancer, 2009, 16, 233-241. | 3.1 | 37 |
| 49 | Equivocal, explicit and emergent actions of PKC isoforms in cancer. Nature Reviews Cancer, 2021, 21, 51-63. | 28.4 | 37 |
| 50 | Molecular Recognition of the Tes LIM2â€“3 Domains by the Actin-related Protein Arp7A. Journal of Biological Chemistry, 2011, 286, 11543-11554. | 3.4 | 36 |
| 51 | Molecular interactions of fission yeast Skp1 and its role in the DNA damage checkpoint. Genes To Cells, 2004, 9, 367-382. | 1.2 | 34 |
| 52 | Structures of the Phactr1 RPEL Domain and RPEL Motif Complexes with G-Actin Reveal the Molecular Basis for Actin Binding Cooperativity. Structure, 2012, 20, 1960-1970. | 3.3 | 32 |
| 53 | The discovery of 2-substituted phenol quinazolines as potent RET kinase inhibitors with improved KDR selectivity. European Journal of Medicinal Chemistry, 2016, 112, 20-32. | 5.5 | 32 |
| 54 | RET Functions as a Dual-Specificity Kinase that Requires Allosteric Inputs from Juxtamembrane Elements. Cell Reports, 2016, 17, 3319-3332. | 6.4 | 28 |

| # | Article | IF | Citations |
|---|---|---|---|
| 55 | Architecture and DNA Recognition Elements of the Fanconi Anemia FANCM-FAAP24 Complex. Structure, 2013, 21, 1648-1658. | 3.3 | 26 |
| 56 | A Cancer-Associated Mutation in Atypical Protein Kinase CÎ¹ Occurs in a Substrate-Specific Recruitment Motif. Science Signaling, 2013, 6, ra82. | 3.6 | 25 |
| 57 | Overcoming inhibitions: subversion of CKI function by viral cyclins. Trends in Biochemical Sciences, 1999, 24, 116-120. | 7.5 | 24 |
| 58 | Fluorescence-based incision assay for human XPFâ€“ERCC1 activity identifies important elements of DNA junction recognition. Nucleic Acids Research, 2012, 40, e101-e101. | 14.5 | 24 |
| 59 | Structures of the human Pals1 PDZ domain with and without ligand suggest gated access of Crb to the PDZ peptide-binding groove. Acta Crystallographica Section D: Biological Crystallography, 2015, 71, 555-564. | 2.5 | 24 |
| 60 | RPEL-family rhoGAPs link Rac/Cdc42 GTP loading to G-actin availability. Nature Cell Biology, 2019, 21, 845-855. | 10.3 | 24 |
| 61 | Cryo-EM structures of the XPF-ERCC1 endonuclease reveal how DNA-junction engagement disrupts an auto-inhibited conformation. Nature Communications, 2020, 11, 1120. | 12.8 | 24 |
| 62 | Phosphorylation of a Distinct Structural Form of Phosphatidylinositol Transfer Protein Î± at Ser166 by Protein Kinase C Disrupts Receptor-mediated Phospholipase C Signaling by Inhibiting Delivery of Phosphatidylinositol to Membranes. Journal of Biological Chemistry, 2004, 279, 47159-47171. | 3.4 | 21 |
| 63 | Activation of the receptor tyrosine kinase RET improves long-term hematopoietic stem cell outgrowth and potency. Blood, 2020, 136, 2535-2547. | 1.4 | 21 |
| 64 | Bioisosteric Discovery of NPA101.3, a Second-Generation RET/VEGFR2 Inhibitor Optimized for Single-Agent Polypharmacology. Journal of Medicinal Chemistry, 2020, 63, 4506-4516. | 6.4 | 20 |
| 65 | Structure-function relationships of growth factors and their receptors. British Medical Bulletin, 1989, 45, 554-569. | 6.9 | 19 |
| 66 | The Rho-family GEF FARP2 is activated by aPKCÎ¹ to control polarity and tight junction formation. Journal of Cell Science, 2019, 132, . | 2.0 | 15 |
| 67 | A winged helix domain in human MUS81 binds DNA and modulates the endonuclease activity of MUS81 complexes. Nucleic Acids Research, 2013, 41, 9741-9752. | 14.5 | 14 |
| 68 | Does Noggin head a new class of Kunitz domain?. Trends in Biochemical Sciences, 1993, 18, 208-209. | 7.5 | 13 |
| 69 | Ankyrin for clues about the function 0fp16INK4a. Nature Structural Biology, 1998, 5, 85-88. | 9.7 | 11 |
| 70 | Exon Skipping in the RET Gene Encodes Novel Isoforms That Differentially Regulate RET Protein Signal Transduction. Journal of Biological Chemistry, 2016, 291, 16249-16262. | 3.4 | 10 |
| 71 | Bimodal regulation of axonal transport by the GDNF-RET signalling axis in healthy and diseased motor neurons. Cell Death and Disease, 2022, 13, . | 6.3 | 9 |
| 72 | A genetically-encoded crosslinker screen identifies SERBP1 as a PKCÎµ substrate influencing translation and cell division. Nature Communications, 2021, 12, 6934. | 12.8 | 7 |

| # | Article | IF | Citations |
|---|---|---|---|
| 73 | A two-site flexible clamp mechanism for RET-GDNF-GFRÎ±1 assembly reveals both conformational adaptation and strict geometric spacing. Structure, 2021, 29, 694-708.e7. | 3.3 | 6 |
| 74 | Structure-activity relationship of the p55 TNF receptor death domain and its lymphoproliferation mutants. FEBS Journal, 2001, 268, 1382-1391. | 0.2 | 5 |
| 75 | Preliminary X-ray analysis of a C2-like domain from protein kinase C-Î´. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 693-696. | 2.5 | 4 |
| 76 | Functional implications of assigned, assumed and assembled PKC structures. Biochemical Society Transactions, 2014, 42, 35-41. | 3.4 | 4 |
| 77 | Discovery of N-Trisubstituted Pyrimidine Derivatives as Type I RET and RET Gatekeeper Mutant Inhibitors with a Novel Kinase Binding Pose. Journal of Medicinal Chemistry, 2022, 65, 1536-1551. | 6.4 | 4 |
| 78 | Co-ordinated control of the Aurora B abscission checkpoint by PKCÎµ complex assembly, midbody recruitment and retention. Biochemical Journal, 2021, 478, 2247-2263. | 3.7 | 3 |
| 79 | Crystallization of the xeroderma pigmentosum group F endonuclease fromAeropyrum pernix. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1658-1661. | 2.5 | 2 |
| 80 | Optimised oligonucleotide substrates to assay XPF-ERCC1 nuclease activity for the discovery of DNA repair inhibitors. Chemical Communications, 2019, 55, 11671-11674. | 4.1 | 2 |
| 81 | Competitive Inhibition of aPKC by Par-3/Bazooka and Other Substrates. Developmental Cell, 2019, 49, 680. | 7.0 | 2 |
| 82 | McDonald and colleagues reply. Trends in Biochemical Sciences, 1993, 18, 425-426. | 7.5 | 1 |
| 83 | Activation of the Receptor Tyrosine Kinase (RET) By GDNF/GFRÎ±1 Improves Cord Blood-Derived HSC in Vitro expansion and In Vivo engraftment. Blood, 2019, 134, 1924-1924. | 1.4 | 0 |